#2

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RAW SEQUENCE LISTING   DATE: 12/06/2001
PATENT APPLICATION: **US/09/990,385**   TIME: 17:15:54

Input Set : **A:\PTO.DC.txt**
Output Set: **N:\CRF3\12062001\I990385.raw**

SEQUENCE LISTING
```
  4 (1) GENERAL INFORMATION:
  5      (i) APPLICANT: Koji YANAI et al.
  6     (ii) TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF
  7                              ISOLATING BETA-FRUCTOFURANOSIDASE GENE, SYSTEM FOR
PRODUCING
  8                              BETA-FRUCTOFURANOSIDASE, AND BETA-FRUCTOFURANOSIDASE
VARIANT
  9    (iii) NUMBER OF SEQUENCES: 35
 10     (iv) CORRESPONDENCE ADDRESS:
 11          (A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 12          (B) STREET: 2033 K Street, N.W., Suite 800
 13          (C) CITY: Washington
 14          (D) STATE: D.C.
 15          (E) COUNTRY: U.S.A.
 16          (F) ZIP: 20006
 17      (v) COMPUTER READABLE FORM:
 18          (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 19          (B) COMPUTER: IBM Compatible
 20          (C) OPERATING SYSTEM: MS-DOS
 21          (D) SOFTWARE: Wordperfect 5.1
 22     (vi) CURRENT APPLICATION DATA:
C--> 23          (A) APPLICATION NUMBER: US/09/990,385
C--> 24          (B) FILING DATE: 10-Sep-1998
 25    (vii) PRIOR APPLICATION DATA:
 26          (A) APPLICATION NUMBER: 09/142,623
 27          (B) FILING DATE: September 10, 1998
 28   (viii) ATTORNEY/AGENT INFORMATION:
 29          (A) NAME: Lee Cheng
 30          (B) REGISTRATION NUMBER: 40,949
 31          (C) REFERENCE/DOCKET NUMBER: 2001-1611
 32     (ix) TELECOMMUNICATION INFORMATION:
 33          (A) TELEPHONE: 202-721-8200
 34          (B) TELEFAX: 202-721-8250
 35 (2) INFORMATION FOR SEQ ID NO: 1:
 36      (i) SEQUENCE CHARACTERISTICS:
 37          (A) LENGTH: 635 amino acid residues
 38          (B) TYPE: amino acid
 39          (C) STRANDEDNESS: Not relevant
W--> 40          (D) TOPOLOGY: Not relevant
 41     (ii) MOLECULE TYPE: protein
 42     (vi) ORIGINAL SOURCE:
 43          (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
 44                        (ATCC 20611)
 45     (ix) FEATURE:
 46          (A) NAME/KEY: mat peptide
 47          (B) LOCATION: 1..635
 48          (C) IDENTIFICATION METHOD: E
```

49   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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```
50 Ser Tyr His Leu Asp Thr Thr Ala Pro Pro Pro Thr Asn Leu Ser Thr
51  1               5               10                  15
52 Leu Pro Asn Asn Thr Leu Phe His Val Trp Arg Pro Arg Ala His Ile
53          20                  25                  30
54 Leu Pro Ala Glu Gly Gln Ile Gly Asp Pro Cys Ala His Tyr Thr Asp
55          35                  40                  45
56 Pro Ser Thr Gly Leu Phe His Val Gly Phe Leu His Asp Gly Asp Gly
57          50                  55                  60
58 Ile Ala Gly Ala Thr Thr Ala Asn Leu Ala Thr Tyr Thr Asp Thr Ser
59  65                  70                  75                  80
60 Asp Asn Gly Ser Phe Leu Ile Gln Pro Gly Gly Lys Asn Asp Pro Val
61                  85                  90                  95
62 Ala Val Phe Asp Gly Ala Val Ile Pro Val Gly Val Asn Asn Thr Pro
63              100                 105                 110
64 Thr Leu Leu Tyr Thr Ser Val Ser Phe Leu Pro Ile His Trp Ser Ile
65              115                 120                 125
66 Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ala Arg Asp
67          130                 135                 140
68 Gly Gly Arg Arg Phe Asp Lys Leu Asp Gln Gly Pro Val Ile Ala Asp
69 145                 150                 155                 160
70 His Pro Phe Ala Val Asp Val Thr Ala Phe Arg Asp Pro Phe Val Phe
71                 165                 170                 175
72 Arg Ser Ala Lys Leu Asp Val Leu Leu Ser Leu Asp Glu Glu Val Ala
73              180                 185                 190
74 Arg Asn Glu Thr Ala Val Gln Gln Ala Val Asp Gly Trp Thr Glu Lys
75          195                 200                 205
76 Asn Ala Pro Trp Tyr Val Ala Val Ser Gly Gly Val His Gly Val Gly
77          210                 215                 220
78 Pro Ala Gln Phe Leu Tyr Arg Gln Asn Gly Gly Asn Ala Ser Glu Phe
79 225                 230                 235                 240
80 Gln Tyr Trp Glu Tyr Leu Gly Glu Trp Trp Gln Glu Ala Thr Asn Ser
81              245                 250                 255
82 Ser Trp Gly Asp Glu Gly Thr Trp Ala Gly Arg Trp Gly Phe Asn Phe
83              260                 265                 270
84 Glu Thr Gly Asn Val Leu Phe Leu Thr Glu Glu Gly His Asp Pro Gln
85          275                 280                 285
86 Thr Gly Glu Val Phe Val Thr Leu Gly Thr Glu Gly Ser Gly Leu Pro
87          290                 295                 300
88 Ile Val Pro Gln Val Ser Ser Ile His Asp Met Leu Trp Ala Ala Gly
89 305                 310                 315                 320
90 Glu Val Gly Val Gly Ser Glu Gln Glu Gly Ala Lys Val Glu Phe Ser
91                 325                 330                 335
92 Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser Ala Tyr Ala Ala
93              340                 345                 350
94 Ala Gly Lys Val Leu Pro Ala Ser Ser Ala Val Ser Lys Thr Ser Gly
95          355                 360                 365
96 Val Glu Val Asp Arg Tyr Val Ser Phe Val Trp Leu Thr Gly Asp Gln
97          370                 375                 380
98 Tyr Glu Gln Ala Asp Gly Phe Pro Thr Ala Gln Gln Gly Trp Thr Gly
```

```
 99 385                 390              395                 400
100 Ser Leu Leu Leu Pro Arg Glu Leu Lys Val Gln Thr Val Glu Asn Val
101               405              410                 415
102 Val Asp Asn Glu Leu Val Arg Glu Glu Gly Val Ser Trp Val Val Gly
103               420              425                 430
104 Glu Ser Asp Asn Gln Thr Ala Arg Leu Arg Thr Leu Gly Ile Thr Ile
105           435              440              445
106 Ala Arg Glu Thr Lys Ala Ala Leu Leu Ala Asn Gly Ser Val Thr Ala
107       450              455              460
108 Glu Glu Asp Arg Thr Leu Gln Thr Ala Ala Val Val Pro Phe Ala Gln
109 465              470              475                 480
110 Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Gln Leu Glu Phe Pro
111               485              490              495
112 Ala Ser Ala Arg Ser Ser Pro Leu Gln Ser Gly Phe Glu Ile Leu Ala
113           500              505              510
114 Ser Glu Leu Glu Arg Thr Ala Ile Tyr Tyr Gln Phe Ser Asn Glu Ser
115       515              520              525
116 Leu Val Val Asp Arg Ser Gln Thr Ser Ala Ala Ala Pro Thr Asn Pro
117       530              535              540
118 Gly Leu Asp Ser Phe Thr Glu Ser Gly Lys Leu Arg Leu Phe Asp Val
119 545              550              555                 560
120 Ile Glu Asn Gly Gln Glu Gln Val Glu Thr Leu Asp Leu Thr Val Val
121               565              570              575
122 Val Asp Asn Ala Val Val Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu
123           580              585              590
124 Ser Thr Trp Ala Arg Ser Trp Tyr Asp Asn Ser Thr Gln Ile Arg Phe
125       595              600              605
126 Phe His Asn Gly Glu Gly Glu Val Gln Phe Arg Asn Val Ser Val Ser
127       610              615              620
128 Glu Gly Leu Tyr Asn Ala Trp Pro Glu Arg Asn
129 625              630              635
132 (2) INFORMATION FOR SEQ ID NO: 2:
133       (i) SEQUENCE CHARACTERISTICS:
134           (A) LENGTH: 1905 base pairs
135           (B) TYPE: Nucleic acid
136           (C) STRANDEDNESS: Double stranded
137           (D) TOPOLOGY: Linear
138      (ii) MOLECULE TYPE: Genomic DNA
139      (vi) ORIGINAL SOURCE:
140           (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
141                         (ATCC 20611)
142      (ix) FEATURE:
143           (A) NAME/KEY: mat peptide
144           (B) LOCATION: 1 .. 1905
145           (C) IDENTIFICATION METHOD: E
146      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
147 TCATACCACC TGGACACCAC GGCCCCGCCG CCGACCAACC TCAGCACCCT CCCCAACAAC    60
148 ACCCTCTTCC ACGTGTGGCG GCCGCGCGCG CACATCCTGC CCGCCGAGGG CCAGATCGGC   120
149 GACCCCTGCG CGCACTACAC CGACCCATCC ACCGGCCTCT TCCACGTGGG GTTCCTGCAC   180
```

RAW SEQUENCE LISTING   DATE: 12/06/2001
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```
150 GACGGGGACG GCATCGCGGG CGCCACCACG GCCAACCTGG CCACCTACAC CGATACCTCC  240
151 GATAACGGGA GCTTCCTGAT CCAGCCGGGC GGGAAGAACG ACCCCGTCGC CGTGTTCGAC  300
152 GGCGCCGTCA TCCCCGTCGG CGTCAACAAC ACCCCCACCT TACTCTACAC CTCCGTCTCC  360
153 TTCCTGCCCA TCCACTGGTC CATCCCCTAC ACCCGCGGCA GCGAGACGCA GTCGTTGGCC  420
154 GTCGCGCGCG ACGGCGGCCG CCGCTTCGAC AAGCTCGACC AGGGCCCCGT CATCGCCGAC  480
155 CACCCCTTCG CCGTCGACGT CACCGCCTTC CGCGATCCGT TTGTCTTCCG CAGTGCCAAG  540
156 TTGGATGTGC TGCTGTCGTT GGATGAGGAG GTGGCGCGGA ATGAGACGGC CGTGCAGCAG  600
157 GCCGTCGATG GCTGGACCGA GAAGAACGCC CCCTGGTATG TCGCGGTCTC TGGCGGGGTG  660
158 CACGGCGTCG GGCCCGCGCA GTTCCTCTAC CGCCAGAACG GCGGGAACGC TTCCGAGTTC  720
159 CAGTACTGGG AGTACCTCGG GGAGTGGTGG CAGGAGGCGA CCAACTCCAG CTGGGGCGAC  780
160 GAGGGCACCT GGGCCGGGCG CTGGGGGTTC AACTTCGAGA CGGGGAATGT GCTCTTCCTC  840
161 ACCGAGGAGG GCCATGACCC CCAGACGGGC GAGGTGTTCG TCACCCTCGG CACGGAGGGG  900
162 TCTGGCCTGC CAATCGTGCC GCAGGTCTCC AGTATCCACG ATATGCTGTG GGCGGCGGGT  960
163 GAGGTCGGGG TGGGCAGTGA GCAGGAGGGT GCCAAGGTCG AGTTCTCCCC CTCCATGGCC 1020
164 GGGTTTCTGG ACTGGGGGGTT CAGCGCCTAC GCTGCGGCGG GCAAGGTGCT GCCGGCCAGC 1080
165 TCGGCGGTGT CGAAGACCAG CGGCGTGGAG GTGGATCGGT ATGTCTCGTT CGTCTGGTTG 1140
166 ACGGGCGACC AGTACGAGCA GGCGGACGGG TTCCCCACGG CCCAGCAGGG GTGGACGGGG 1200
167 TCGCTGCTGC TGCCGCGCGA GCTGAAGGTG CAGACGGTGG AGAACGTCGT CGACAACGAG 1260
168 CTGGTGCGCG AGGAGGGCGT GTCGTGGGTG GTGGGGGGAGT CGGACAACCA GACGGCCAGG 1320
169 CTGCGCACGC TGGGGATCAC GATCGCCCGG GAGACCAAGG CGGCCCTGCT GGCCAACGGC 1380
170 TCGGTGACCG CGGAGGAGGA CCGCACGCTG CAGACGGCGG CCGTCGTGCC GTTCGCGCAA 1440
171 TCGCCGAGCT CCAAGTTCTT CGTGCTGACG GCCCAGCTGG AGTTCCCCGC GAGCGCGCGC 1500
172 TCGTCCCCGC TCCAGTCCGG GTTCGAAATC CTGGCGTCGG AGCTGGAGCG CACGGCCATC 1560
173 TACTACCAGT TCAGCAACGA GTCGCTGGTC GTCGACCGCA GCCAGACTAG TGCGGCGGCG 1620
174 CCCACGAACC CCGGGCTGGA TAGCTTTACT GAGTCCGGCA AGTTGCGGTT GTTCGACGTG 1680
175 ATCGAGAACG GCCAGGAGCA GGTCGAGACG TTGGATCTCA CTGTCGTCGT GGATAACGCG 1740
176 GTTGTCGAGG TGTATGCCAA CGGGCGCTTT GCGTTGAGCA CCTGGGCGAG ATCGTGGTAC 1800
177 GACAACTCCA CCCAGATCCG CTTCTTCCAC AACGGCGAGG GCGAGGTGCA GTTCAGGAAT 1860
178 GTCTCCGTGT CGGAGGGGCT CTATAACGCC TGGCCGGAGA GAAAT                1905
180 (2) INFORMATION FOR SEQ ID NO: 3:
181      (i) SEQUENCE CHARACTERISTICS:
182          (A) LENGTH: 20 amino acid residues
183          (B) TYPE: Amino acid
184          (C) STRANDEDNESS: Not relevant
185          (D) TOPOLOGY: Linear
186     (ii) MOLECULE TYPE: Peptide
187      (v) FRAGMENT TYPE: internal fragment
188     (vi) ORIGINAL SOURCE:
189          (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
190                       (ATCC 20611)
191     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
192 Leu Asp Gln Gly Pro Val Ile Ala Asp His Pro Phe Ala Val Asp Val
193  1              5                  10                  15
194 Thr Ala Phe Arg
195            20
197 (2) INFORMATION FOR SEQ ID NO: 4:
198      (i) SEQUENCE CHARACTERISTICS:
199          (A) LENGTH: 20 amino acid residues
200          (B) TYPE: Amino acid
```

```
201              (C) STRANDEDNESS: Not relevant
202              (D) TOPOLOGY: Linear
203        (ii) MOLECULE TYPE: Peptide
204         (v) FRAGMENT TYPE: internal fragment
205        (vi) ORIGINAL SOURCE:
206              (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
207                      (ATCC 20611)
208        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
209 Val Glu Phe Ser Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser
210   1               5                  10                  15
211 Ala Tyr Ala Ala
212              20
214 (2) INFORMATION FOR SEQ ID NO: 5:
215        (i) SEQUENCE CHARACTERISTICS:
216              (A) LENGTH: 20 amino acid residues
217              (B) TYPE: Amino acid
218              (C) STRANDEDNESS: Not relevant
219              (D) TOPOLOGY: Linear
220        (ii) MOLECULE TYPE: Peptide
221         (v) FRAGMENT TYPE: internal fragment
222        (vi) ORIGINAL SOURCE:
223              (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
224                      (ATCC 20611)
225        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
226 Val Gln Thr Val Glu Asn Val Val Asp Asn Glu Leu Val Arg Glu Glu
227   1               5                  10                  15
228 Gly Val Ser Trp
229              20
231 (2) INFORMATION FOR SEQ ID NO: 6:
232        (i) SEQUENCE CHARACTERISTICS:
233              (A) LENGTH: 20 amino acid residues
234              (B) TYPE: Amino acid
235              (C) STRANDEDNESS: Not relevant
236              (D) TOPOLOGY: Linear
237        (ii) MOLECULE TYPE: Peptide
238         (v) FRAGMENT TYPE: internal fragment
239        (vi) ORIGINAL SOURCE:
240              (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
241                      (ATCC 20611)
242        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
W--> 243 Ala Ala Leu Leu Ala Xaa Gly Ser Val Thr Ala Glu Glu Asp Arg Thr
244   1               5                  10                  15
245 Leu Gln Thr Ala
246              20
248 (2) INFORMATION FOR SEQ ID NO: 7:
249        (i) SEQUENCE CHARACTERISTICS:
250              (A) LENGTH: 6 amino acid residues
251              (B) TYPE: Amino acid
252              (C) STRANDEDNESS: Not relevant
```

VERIFICATION SUMMARY   DATE: 12/06/2001
PATENT APPLICATION: **US/09/990,385**   TIME: 17:15:55

Input Set : **A:\PTO.DC.txt**
Output Set: **N:\CRF3\12062001\I990385.raw**

```
L:23  M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:24  M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:40  M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:269 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:279 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:356 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=11
L:487 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:621 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:631 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:641 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:651 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18
L:661 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:671 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:681 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:691 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:701 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:711 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:721 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:731 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:741 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:751 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:761 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:771 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:781 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:791 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:801 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:811 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:821 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
```